

#11

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1636

RAW SEQUENCE TECH CENTER

PATENT APPLICATION: US/09/659,737A

DATE: 02/26/2002

TIME: 13:59:19

Input Set : A:\71369-172(PFI-024US).ST25.txt

Output Set: N:\CRF3\02262002\I659737A.raw

3 <110> APPLICANT: Blumenberg, Miroslav
 4 Gazel, Alix M.
 6 <120> TITLE OF INVENTION: Genes and Polynucleotides Associated with Ultraviolet
 7 Radiation-Mediated Skin Damage and Uses Thereof
 9 <130> FILE REFERENCE: 71369.172(PFI-024US)
 11 <140> CURRENT APPLICATION NUMBER: US 09/659,737A
 12 <141> CURRENT FILING DATE: 2000-09-11
 14 <150> PRIOR APPLICATION NUMBER: US 60/155,029
 15 <151> PRIOR FILING DATE: 1999-09-20
 17 <160> NUMBER OF SEQ ID NOS: 19
 19 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 164
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Homo sapiens
 26 <220> FEATURE:
 27 <221> NAME/KEY: CDS
 28 <222> LOCATION: (2)...(163)
 30 <400> SEQUENCE: 1
 31 g cac cgg gac atc aag gca gga aat att ttg cta ctt gag aag ata gaa 49
 32 His Arg Asp Ile Lys Ala Gly Asn Ile Leu Leu Leu Glu Lys Ile Glu
 33 1 5 10 15
 35 cat gat gac atc tgc aat aaa act ttg aag att aca gat ttt ggg ttg 97
 36 His Asp Asp Ile Cys Asn Lys Thr Leu Lys Ile Thr Asp Phe Gly Leu
 37 20 25 30
 39 gcg agg gaa tgg cac agg acc acc aaa atg agc aca gca ggc acc tat 145
 40 Ala Arg Glu Trp His Arg Thr Thr Lys Met Ser Thr Ala Gly Thr Tyr
 41 35 40 45
 43 gcc tgg atg gcc cca gaa g
 44 Ala Trp Met Ala Pro Glu 164
 45 50
 48 <210> SEQ ID NO: 2
 49 <211> LENGTH: 54
 50 <212> TYPE: PRT
 51 <213> ORGANISM: Homo sapiens
 53 <400> SEQUENCE: 2
 54 His Arg Asp Ile Lys Ala Gly Asn Ile Leu Leu Leu Glu Lys Ile Glu
 55 1 5 10 15
 56 His Asp Asp Ile Cys Asn Lys Thr Leu Lys Ile Thr Asp Phe Gly Leu
 57 20 25 30
 58 Ala Arg Glu Trp His Arg Thr Thr Lys Met Ser Thr Ala Gly Thr Tyr
 59 35 40 45
 60 Ala Trp Met Ala Pro Glu

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Input Set : A:\71369-172(PFI-024US).ST25.txt
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61      50
64 <210> SEQ ID NO: 3
65 <211> LENGTH: 145
66 <212> TYPE: DNA
67 <213> ORGANISM: Homo sapiens
69 <220> FEATURE:
70 <221> NAME/KEY: CDS
71 <222> LOCATION: (2)...(145)
73 <400> SEQUENCE: 3
74 a cat cgg gac atc aag agc gac tcg atc ctg acc cat gat ggc agg 49
75 His Arg Asp Ile Lys Ser Asp Ser Ile Leu Leu Thr His Asp Gly Arg
76    1           5           10          15
78 gtg aag ctg tca gac ttt ggg ttc tgc gcc cag gtg agc aag gaa gtg  97
79 Val Lys Leu Ser Asp Phe Gly Phe Cys Ala Gln Val Ser Lys Glu Val
80        20          25          30
82 ccc cga agg aag tcg ctg gtc ggc acg ccc tac tgg atg gcc cca gag 145
83 Pro Arg Arg Lys Ser Leu Val Gly Thr Pro Tyr Trp Met Ala Pro Glu
84        35          40          45
88 <210> SEQ ID NO: 4
89 <211> LENGTH: 48
90 <212> TYPE: PRT
91 <213> ORGANISM: Homo sapiens
93 <400> SEQUENCE: 4
94 His Arg Asp Ile Lys Ser Asp Ser Ile Leu Leu Thr His Asp Gly Arg
95    1           5           10          15
96 Val Lys Leu Ser Asp Phe Gly Phe Cys Ala Gln Val Ser Lys Glu Val
97        20          25          30
98 Pro Arg Arg Lys Ser Leu Val Gly Thr Pro Tyr Trp Met Ala Pro Glu
99        35          40          45
102 <210> SEQ ID NO: 5
103 <211> LENGTH: 146
104 <212> TYPE: DNA
105 <213> ORGANISM: Homo sapiens
107 <220> FEATURE:
108 <221> NAME/KEY: CDS
109 <222> LOCATION: (2)...(145)
111 <400> SEQUENCE: 5
112 t cac agg gac atc aag agt gac tcc atc ctg ctg acc ctc gat ggc agg 49
113 His Arg Asp Ile Lys Ser Asp Ser Ile Leu Leu Thr Leu Asp Gly Arg
114    1           5           10          15
116 gtg aag ctc tcg gac ttc gga ttc tgt gct cag atc agc aaa gac gtc  97
117 Val Lys Leu Ser Asp Phe Gly Phe Cys Ala Gln Ile Ser Lys Asp Val
118        20          25          30
120 cct aag agg aag tcc ctg gtg gga acc ccc tac tgg atg gcg ccc gag 145
121 Pro Lys Arg Lys Ser Leu Val Gly Thr Pro Tyr Trp Met Ala Pro Glu
122        35          40          45
124 g
126 <210> SEQ ID NO: 6
127 <211> LENGTH: 48

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Input Set : A:\71369-172(PFI-024US).ST25.txt
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128 <212> TYPE: PRT
129 <213> ORGANISM: Homo sapiens
131 <400> SEQUENCE: 6
132 His Arg Asp Ile Lys Ser Asp Ser Ile Leu Leu Thr Leu Asp Gly Arg
133 1 5 10 15
134 Val Lys Leu Ser Asp Phe Gly Phe Cys Ala Gln Ile Ser Lys Asp Val
135 20 25 30
136 Pro Lys Arg Lys Ser Leu Val Gly Thr Pro Tyr Trp Met Ala Pro Glu
137 35 40 45
140 <210> SEQ ID NO: 7
141 <211> LENGTH: 3627
142 <212> TYPE: DNA
143 <213> ORGANISM: Homo sapiens
145 <220> FEATURE:
146 <221> NAME/KEY: CDS
147 <222> LOCATION: (868)..(1275)
149 <220> FEATURE:
150 <221> NAME/KEY: CDS
151 <222> LOCATION: (1420)..(1553)
153 <220> FEATURE:
154 <221> NAME/KEY: CDS
155 <222> LOCATION: (1900)..(2026)
157 <220> FEATURE:
158 <221> NAME/KEY: CDS
159 <222> LOCATION: (2105)..(2230)
161 <220> FEATURE:
162 <221> NAME/KEY: CDS
163 <222> LOCATION: (2696)..(2833)
165 <400> SEQUENCE: 7
166 gatctgcac ctccttcaga acctgccaaa atgacttagga aaaatgctgt ttccatagca 60
167 agagccaaa gagaacatga cggccctgca ctccgggatc tctctggcac cagattccca 120
168 gcccaggaa gacacctgaa ccccccagat ggtgacacac ctctgtggtc ctctgtcagg 180
169 gacataacct cccagcacag atttgcAACAC tccctgctgc aggcacaAGC aggctatcg 240
170 ggccccaggt gtggctcccc tgccttgggtt cagggagtgg agacacagtt gcccactgct 300
171 ccccaaaaaa ctgcaggccc tcttctgccc ccattgggtcc tgggggtgggg gagccttggg 360
172 agttgaagaa tgcctctgac ccagattttt caagcagcct ctgagctcag aggaagagtc 420
173 tgcctcacgg cagcctccct ggggtcttagc tgtcaatcgc ccaggaagaa ataccagcg 480
174 cggggacccgg cggggaaagct ggccttctt gtctcccag gtgcagcaca gcgagtgtaa 540
175 ggagctgtct tgggcctgccc cagcctgggt ccctgcgggg gactgctggc acaggactgt 600
176 gactgggctt cagctctgac tgaaaatctt tgcttcagag cacctccca gtttgatctg 660
177 ataccccgcc tgaccctgccc agagtccaga ggtcacggcg gccagccct gcctccggga 720
178 aggttattcc aaatgctccc acagccctga cccttcctgt tgcttggtcc cttgcagccc 780
179 aactcctctt tccgaccggcc gcagaaagac aaccccccac gcctggtggc caaggcccag 840
180 tccttgcctt cggaccagcc ggtgggg acc ttc agc cct ctg acc act tcg gat 894
181 1 5
182 Thr Phe Ser Pro Leu Thr Thr Ser Asp
184 acc agc agc ccc cag aag tcc ctc cgc aca gcc ccg gcc aca ggc cag 942
185 Thr Ser Ser Pro Gln Lys Ser Leu Arg Thr Ala Pro Ala Thr Gly Gln
186 10 15 20 25

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188 ctt cca ggc cgg tct tcc cca gcg gga tcc ccc cgc acc tgg cac gcc	990
189 Leu Pro Gly Arg Ser Ser Pro Ala Gly Ser Pro Arg Thr Trp His Ala	
190 30 35 40	
192 cag atc agc acc agc aac ctg tac ctg ccc cag gac ccc acg gtt gcc	1038
193 Gln Ile Ser Thr Ser Asn Leu Tyr Leu Pro Gln Asp Pro Thr Val Ala	
194 45 50 55	
196 aag ggt gcc ctg gct ggt gag gac aca ggt gtt gtg aca cat gag cag	1086
197 Lys Gly Ala Leu Ala Gly Glu Asp Thr Gly Val Val Thr His Glu Gln	
198 60 65 70	
200 ttc aag gct gcg ctc agg atg gtg gac cag ggt gac ccc cgg ctg	1134
201 Phe Lys Ala Ala Leu Arg Met Val Val Asp Gln Gly Asp Pro Arg Leu	
202 75 80 85	
204 ctg ctg gac agc tac gtg aag att ggc gag ggc tcc acc ggc atc gtc	1182
205 Leu Leu Asp Ser Tyr Val Lys Ile Gly Glu Gly Ser Thr Gly Ile Val	
206 90 95 100 105	
208 tgc ttg gcc cgg gaa gaa cac tcg ggc cgc cag gtg gcc gtc aag atg	1230
209 Cys Leu Ala Arg Glu Glu His Ser Gly Arg Gln Val Ala Val Lys Met	
210 110 115 120	
212 atg gac ctc aga aag cag cag cgc agg gag ctg ctc ttc aac gag	1275
213 Met Asp Leu Arg Lys Gln Gln Arg Arg Glu Leu Leu Phe Asn Glu	
214 125 130 135	
216 gtggggaggac agggtgggac acacacgggg gcgttgggta tggcagtga gcagccagcc	1335
217 aggctggaca tctgtgagca ggggcagtgg gtggccatgc gtctggcac tgcctggc	1395
218 actcaggccc ccacctgccc ccag gtg atc atg cgg gac tac cag cac	1446
219 Val Val Ile Met Arg Asp Tyr Gln His	
220 140 145	
222 ttc aac gtg gtg gag atg tac aag agc tac ctg gtg ggc gag gag ctg	1494
223 Phe Asn Val Val Glu Met Tyr Lys Ser Tyr Leu Val Gly Glu Glu Leu	
224 150 155 160	
226 tgg gtg ctc atg gag ttc ctg cag gga gga gcc ctc aca gac atc gtc	1542
227 Trp Val Leu Met Glu Phe Leu Gln Gly Gly Ala Leu Thr Asp Ile Val	
228 165 170 175	
230 tcc caa gtc ag gtggcagct gggaggcgtg gaccctgagt gcaggctgcc	1593
231 Ser Gln Val Arg	
232 180	
234 ctcaccatgg ccctgccagg gcaatgtggt cttctgcctg tggcccagaa gacttgggat	1653
235 gcctgggctc ccctgcctgc tggggtaact gagacccagg ggtcttggga gtggagaaga	1713
236 gaaggatagc ttctagccaa agctcaggcc ccagtttca ccaggcgtat ggcctgactg	1773
237 tgctgccaaa cagattgcct gggagctgtg gggcttagca ccagggactc ctactctgct	1833
238 cagccaccccc acgacactgcc agagctaacg ttctcttca tcgggtggcc ccaccttccct	1893
239 gtccag g ctg aat gag gag cag att gcc act gtg tgt gag gct gtg ctg	1942
240 Leu Asn Glu Glu Gln Ile Ala Thr Val Cys Glu Ala Val Leu	
241 185 190 195	
243 cag gcc ctg gcc tac ctg cat gct cag ggt gtc atc cac cgg gac atc	1990
244 Gln Ala Leu Ala Tyr Leu His Ala Gln Gly Val Ile His Arg Asp Ile	
245 200 205 210	
247 aag agt gac tcc atc ctg ctg acc ctc gat ggc agg gtaggtccca	2036
248 Lys Ser Asp Ser Ile Leu Leu Thr Leu Asp Gly Arg	
249 215 220	

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251	tcctgtccct	ggcacagcca	cgctccact	tcctcctgat	ccaccactca	ctccctttc	2096											
252	aaccgcag	gtg	aag	ctc	tcg	gac	ttc	tgc	cgt	cag	atc	agc	aaa	2146				
253	Val	Lys	Leu	Ser	Asp	Phe	Gly	Phe	Cys	Ala	Gln	Ile	Ser	Lys				
254	225						230							235				
255	gac	gtc	cct	aag	agg	aag	tcc	ctg	gtg	gga	acc	ccc	tac	tgg	atg	gct	2194	
256	Asp	Val	Pro	Lys	Arg	Lys	Ser	Leu	Val	Gly	Thr	Pro	Tyr	Trp	Met	Ala		
257	240						245							250				
258	cct	gaa	gtg	atc	tcc	agg	tct	ttg	tat	gcc	act	gag	gttaaccgttc	2240				
259	Pro	Glu	Val	Ile	Ser	Arg	Ser	Leu	Tyr	Ala	Thr	Glu						
260	255						260							265				
261	cctccacccc	ccagacctcc	caaaagcaac	ttggcaactg	gcagctcttc	tgctgtggcc	2300											
262	cctccagtga	gctcacaaa	agcagccctg	gttttcagag	tcccacccat	tcaacaccct	2360											
263	tcccccttcc	gatggggctg	ctcttaccca	gtgactttgc	tgccaggaac	gagtcctgca	2420											
264	agtgcattcc	tcagctcaag	ggcagaatgg	ggtatggccg	ggcctccat	gtatgtggc	2480											
265	ctttctctga	gtgactgaca	gtctgttccc	tataggcagt	ggtcactcat	gcagggcagta	2540											
266	actggccaca	gggcaggtga	ccaggggagg	aaggagacag	acccaccaag	gagagctggg	2600											
267	gcccagtc	ccccctccac	cactgctgcc	accagaacgc	agctaccaat	ggggcaggg	2660											
268	ctggccatgg	ggtcagggac	attttcctcc	tgcag	gtg	atc	tgg	tct	ctg	2713								
269										Val	Asp	Ile	Trp	Ser	Leu			
270										270								
271	275	ggg	atc	atg	gtg	att	gag	atg	gta	gat	ggg	gag	cca	ccg	tac	ttc	agt	2761
272	Gly	Ile	Met	Val	Ile	Glu	Met	Val	Asp	Gly	Glu	Pro	Pro	Tyr	Phe	Ser		
273	275						280							285				
274	gac	tcc	cca	gtg	caa	gcc	atg	aag	agg	ctc	cg	gac	agc	ccc	cca	ccc	2809	
275	Asp	Ser	Pro	Val	Gln	Ala	Met	Lys	Arg	Leu	Arg	Asp	Ser	Pro	Pro	Pro		
276	290						295							300				
277	290	aag	ctg	aaa	aac	tct	cac	aag	gtc	agttggcaca	caagggtgcg	acctcgcaga	2863					
278	Lys	Leu	Lys	Asn	Ser	His	Lys	Val										
279	295	305					310											
280	ccccattcct	cctgaggcaa	ggggaccaga	acctgggctc	ccagcatctc	ccttccactg	2923											
281	aagccacagg	gtctgggctc	ctggaaaagg	ctcccttcc	cccacacaaa	acccgcac	2983											
282	gggtgtggag	ccgcatactac	gcacaagttc	gcatgtgcgc	tccgacaagt	cgcctccac	3043											
283	ggctgtggca	ggagagttgc	tgcttggcag	aagggttgc	gcttggcagg	cactggtcgg	3103											
284	aagcccagtg	gggcccattga	gcagggaaag	ccagcacacc	agcaactccc	tgctgtccag	3163											
285	ggagggatcc	ggagaagctt	cactgagcac	aaacccttca	acccgtgtcg	ggagatccat	3223											
286	accatgatcc	gatgtccctg	tccatcacgg	cgagtcggct	catgctccat	tcgttgtcaca	3283											
287	ccccgacaca	gctaagccac	agcgttcccc	ttaaagccag	tataagtgc	tggaagtgg	3343											
288	atacatgtaa	cccttttgc	caaatcgccc	ccaaaaaccgc	aggcctact	gtggacgccc	3403											
289	cctgtggca	ggtcagcacg	gggctgataa	gtggcaccgc	catctggtgg	ccaaaacaag	3463											
290	aaatgtctca	gagggctgaa	gcctctcc	taaaatagca	aaaaaacaag	agttctgtgg	3523											
291	cccccaacaca	aagctggatg	ggaggaccaa	cagaaaacat	cttccaagac	aactggct	3583											
292	tggagccgc	accgctaacc	ccaaaattag	catataaagc	atgc		3627											
293	<210>	SEQ ID NO:	8															
294	<211>	LENGTH:	311															
295	<212>	TYPE:	PRT															
296	<213>	ORGANISM:	Homo sapiens															
297	<400>	SEQUENCE:	8															
298	308	Thr	Phe	Ser	Pro	Leu	Thr	Thr	Ser	Asp	Thr	Ser	Ser	Pro	Gln	Lys	Ser	
299	309	1					5				10				15			

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\71369-172(PFI-024US).ST25.txt
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L:660 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:1021 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:1034 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:1047 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:1060 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17